SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: AMGEN INC.
- (ii) TITLE OF INVENTION: TRUNCATED SOLUBLE TUMOR NECROSIS FACTOR
 TYPE-I AND TYPE-II RECEPTORS
- (iii) NUMBER OF SEQUENCES: 81
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: AMGEN INC.
 - (B) STREET: 1840 De Havilland Drive
 - (C) CITY: Thousand Oaks
 - (D) STATE: California
 - (E) COUNTRY: US
 - (F) ZIP: 91320-1789
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/021,443
 - (B) FILING DATE: 09-JUL-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/032,534
 - (B) FILING DATE: 06-DEC-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/037,737
 - (B) FILING DATE: 23-JAN-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/039,314
 - (B) FILING DATE: 07-FEB-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/039,792
 - (B) FILING DATE: 04-MAR-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Zindrick, Thomas D.
 - (B) REGISTRATION NUMBER: 32,185
 - (C) REFERENCE/DOCKET NUMBER: A-415E

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 483 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown

- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | (xi) | SEÇ | QUENC | CE DE | ESCR | PTIC | ON: S | SEQ 1 | ID NO | 0:1: | | | | |
|------------|------|-----|-------|------------------|------|------|-------|-------|-------|------|--|--|-----|---|
| _ | - | | | CCC Pro 5 | | | | | | | | | 4 8 | 3 |
| | | | | AAG Lys | | | | | | | | | 96 | õ |
| | | | | CAG Gln | | | | | | | | | 144 | 1 |
| | | | | GAA Glu | | | | | | | | | 192 | 2 |
| | | | | ATG Met | | | | | | | | | 240 |) |
| | | | | TGT Cys 85 | | | | | | | | | 288 | 3 |
| | - | | | TTC Phe | | | | | | | | | 336 | 5 |
| | | | | TCC Ser | | | | | | | | | 384 | 1 |
| | | | | TTT Phe | | | | | | | | | 432 | 2 |
| | | | | CTG Leu | | | | | | | | | 480 |) |
| AAT Asn | | | | | | | | | | | | | 483 | 3 |

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 161 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser 1 5 10 15

Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys
20 25 30

Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser 35 40 45

Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys 50 55 60

Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp 65 70 75 80

Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp 85 90 95

Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly 100 105 110

Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys 115 120 125

His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn 130 135 140

Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu 145 150 155 160

Asn

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 332 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 4..324

| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: | |
|---|-------|
| CAT ATG GAC AGC GTT TGC CCC CAA GGA AAA TAC ATC CAC CCT CAA AA' Met Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Ass | n |
| AAT TCG ATT TGC TGT ACC AAG TGC CAC AAA GGA ACC TAC TTG TAC AA' Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Ass 20 25 30 | |
| GAC TGT CCA GGC CCG GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGG Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Se 35 40 45 | C 144 |
| GGC TCC TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGG Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cy. 50 55 60 | |
| TCC AAA TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC AC. Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Th 65 70 75 | |
| GTG GAC CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CA Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg Hi 80 85 90 9 | s |
| TAT TGG AGT GAA AAC CTT TTC CAG TGC TTC TGC TGA TAGGATCC Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Cys * 100 105 | 332 |
| (2) INFORMATION FOR SEQ ID NO:4: | |
| (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 107 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear | |
| (ii) MOLECULE TYPE: protein | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4: | |
| Met Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn As 1 5 10 15 | n |
| Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn As 20 25 30 | p |
| Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gl 35 40 45 | У |
| Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Se 50 55 60 | r |
| Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Va 65 70 75 8 | |

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Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Cys * 100 (2) INFORMATION FOR SEQ ID NO:5: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 339 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 4..333 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5: CAT ATG GAC AGC GTT TGC CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT Met Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn AAT TCG ATT TGC TGT ACC AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT 96 Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn 20 GAC TGT CCA GGC CCG GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC 144 Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser GGC TCC TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC 192 Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys TCC AAA TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA 240 Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr 288 GTG GAC CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His 80

TAT TGG AGT GAA AAC CTT TTC CAG TGC TTC AAT TGC TCT CTG TAA Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu *

AAGCTT

105

333

339

110

(2) INFORMATION FOR SEQ ID NO:6:

| | | (i) | (A (B |) LE) TY | CHA NGTH PE: POLO | : 11 amin | 0 am o ac | ino id | | s | | | | | | |
|------------|-----------------|--------------------|----------------------------------|----------------------|---|-------------------------------|-------------------------------|------------|------------------|------------------|------------|------------|------------|------------------|------------------|----|
| | (: | ii) | MOLE | CULE | TYP | E: p | rote | in | | | | | | | | |
| | (: | xi) | SEQU | ENCE | DES | CRIP | TION | : SE | Q ID | NO: | 6: | | | | | |
| Met 1 | Asp | Ser | Val | Cys 5 | Pro | Gln | Gly | Lys | Tyr 10 | Ile | His | Pro | Gln | Asn 15 | Asn | |
| Ser | Ile | Cys | Cys 20 | Thr | Lys | Cys | His | Lys 25 | Gly | Thr | Tyr | Leu | Tyr 30 | Asn | Asp | |
| Cys | Pro | Gly 35 | Pro | Gly | Gln | Asp | Thr 40 | Asp | Cys | Arg | Glu | Cys 45 | Glu | Ser | Gly | |
| Ser | Phe 50 | Thr | Ala | Ser | Glu | Asn 55 | His | Leu | Arg | His | Cys 60 | Leu | Ser | Cys | Ser | |
| Lys 65 | Cys | Arg | Lys | Glu | Met 70 | Gly | Gln | Val | Glu | Ile 75 | Ser | Ser | Cys | Thr | Val 80 | |
| Asp | Arg | Asp | Thr | Val 85 | Cys | Gly | Cys | Arg | Lys 90 | Asn | Gln | Tyr | Arg | His 95 | Tyr | |
| Trp | Ser | Glu | Asn 100 | Leu | Phe | Gln | Cys | Phe 105 | Asn | Cys | Ser | Leu | * 110 | | | |
| (2) | INFO | ORMA: | rion | FOR | SEQ | ID i | 10:7 | : | | | | | | | | |
| | | () () () | A) LE B) TY C) ST O) TO | ENGTI PE: PANI | HARAC H: 33 nucl DEDNE DGY: | 33 ba Leic ESS: unkr | ase p acid unkr nown | pairs i | 3 | | | | | | | |
| | (ii) | MOI | LECUI | LE T | YPE: | CDNA | J | | | | | | | | | |
| | (ix) | (F | | AME/F | KEY: ION: | | 324 | | | | | | | | | |
| | (xi) | SEÇ | UENC | E DE | ESCRI | PTIC | n: s | SEQ I | D NO |):7: | | | | | | |
| CAT | ATG Met 1 | GAC A sp | AGC Ser | GTT Val | TGC Cys 5 | CCC Pro | CAA Gln | GGA Gly | AAA Lys | TAT Tyr 10 | ATC Ile | CAC His | CCT Pro | CAA Gln | AAT Asn 15 | 48 |
| AAT Asn | TCG Ser | ATT Ile | TGC Cys | TGT Cys 20 | ACC Thr | AA G Lys | TGC Cys | CAC His | AAA Lys 25 | GGA Gly | ACC Thr | TAC Tyr | TTG Leu | TAC Tyr 30 | AAT Asn | 96 |

| GAC TGT CCA GGC CCG GG Asp Cys Pro Gly Pro Gl 35 | G CAG GAT ACG y Gln Asp Thr | GAC TGC AGG GAG TGT (Asp Cys Arg Glu Cys (45 | SAG AGC 144 Slu Ser |
|--|--|--|------------------------|
| GGC TCC TTC ACC GCT TC Gly Ser Phe Thr Ala Se 50 | A GAA AAC CAC r Glu Asn His 55 | CTC AGA CAC TGC CTC : Leu Arg His Cys Leu : 60 | AGC TGC 192 Ser Cys |
| TCC AAA TGC CGA AAG GA Ser Lys Cys Arg Lys Gl 65 | A ATG GGT CAG u Met Gly Gln 70 | GTG GAG ATC TCT TCT 'Val Glu Ile Ser Ser (| CGC ACA 240 Cys Thr |
| GTG GAC CGG GAC ACC GT Val Asp Arg Asp Thr Va 80 8 | | | |
| TAT TGG AGT GAA AAC CT Tyr Trp Ser Glu Asn Le 100 | u Phe Gln Cys | | 333 . |
| (B) TYPE: | ARACTERISTICS: H: 107 amino a amino acid OGY: linear | cids | |
| (xi) SEQUENCE DE | SCRIPTION: SEQ | ID NO:8: | |
| Met Asp Ser Val Cys Pr 1 5 | o Gln Gly Lys | Tyr Ile His Pro Gln . 10 | Asn Asn 15 |
| Ser Ile Cys Cys Thr Ly 20 | rs Cys His Lys 25 | Gly Thr Tyr Leu Tyr . | Asn Asp |
| Cys Pro Gly Pro Gly Gl 35 | n Asp Thr Asp | Cys Arg Glu Cys Glu 45 | Ser Gly |
| Ser Phe Thr Ala Ser Gl 50 | u Asn His Leu 55 | Arg His Cys Leu Ser | Cys Ser |
| | | | |
| Lys Cys Arg Lys Glu Me 65 7 | t Gly Gln Val | Glu Ile Ser Ser Cys 75 | Thr Val 80 |

Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn * 100 105

(2) INFORMATION FOR SEQ ID NO:9:

| (2) | INFO | KMAT | TON | FOR | SEQ | ID N | 10.9. | | | | | | | | | |
|------------|------------------|----------------|------------------------|---------------------|----------------------|------------------------------------|----------------------|------------------|------------------|------------|------------|------------|------------------|------------------|------------|-----|
| | (i) | (A (B (C |) LE () TY () SI | NGTH PE: RANE | : 28 nucl EDNE | TERI 5 ba eic SS: unkr | se p acio unkr | oairs 1 | 3 | | | | | | | |
| | (ii) | MOI | ECUI | E TY | PE: | CDNA | A | | | | | | | | | |
| | (ix) | (P |) NA | ME/F | KEY: | CDS 42 | 279 | | | | | | | | | |
| | (xi) | SEÇ | UENC | CE DE | ESCRI | PTIC | ON: S | SEQ : | ID NO |):9: | | | | | | |
| CAT | ATG Met 0 | | | | | | | | | | | | | | | 48 |
| CCA Pro | GGC (| CCG Pro | GGG Gly | CAG Gln 20 | GAT Asp | ACG Thr | GAC Asp | TGC Cys | AGG Arg 25 | GAG Glu | TGT Cys | GAG Glu | AGC Ser | GGC Gly 30 | TCC Ser | 96 |
| TTC Phe | ACC f | GCT Ala | TCA Ser 35 | GAA Glu | AAC Asn | CAC His | CTC Leu | AGA Arg 40 | CAC His | TGC Cys | CTC Leu | AGC Ser | TGC Cys 45 | TCC Ser | AAA Ĺys | 144 |
| | CGA . | | | | | | | | | | | | | | | 192 |
| | GAC Asp 65 | | | | | | | | | | | | | | | 240 |
| | GAA Glu | | | | | | | | | | | | AAG | CTT | | 285 |
| (2) | INFO | RMA: | rion | FOR | SEQ | ID 1 | NO:1 | 0: | | | | | | | | |
| | (| | (A) | LEI TYI | NGTH PE: a | RACTI : 92 amin GY: | ami o ac | no a id | | | | | | | | |
| | (i | i) 1 | MOLE | CULE | TYP | E: p | rote | in | | | | | | | | |
| | (x | i) : | SEQUI | ENCE | DES | CRIP' | TION | : SE | Q ID | NO: | 10: | | | | | |
| Met 1 | Cys | Thr | Lys | Cys 5 | His | Lys | Gly | Thr | Tyr 10 | Leu | Tyr | Asn | Asp | Cys 15 | Pro | |
| Gly | Pro | Gly | Gln 20 | Asp | Thr | Asp | Cys | Arg 25 | Glu | Cys | Glu | Ser | Gly 30 | Ser | Phe | |

| Thr | Ala | Ser 35 | | Asn | His | Leu | Arg 40 | His | Суз | Leu | Ser | Cys 45 | Ser | Lys | Cys | |
|------------------|------------------|-------------------|--------------------------------------|------------------------------|------------------------------|--------------------------------|---------------------------------------|--------------|------------------|------------------|------------------|------------|------------|------------------|------------------|-----|
| Arg | Lys 50 | Glu | Met | Gly | Gln | Val 55 | Glu | Ile | Ser | Ser | Cys 60 | Thr | Val | Asp | Arg | |
| Asp 65 | Thr | Val | Cys | Gly | Cys 70 | Arg | Lys | Asn | Gln | Туг 75 | Arg | His | Туr | Trp | Ser 80 | |
| Glu | Asn | Leu | Phe | Gln 85 | Cys | Phe | Asn | Cys | Ser 90 | Leu | * | | | | | |
| (2) | (i |) SE(() () | QUEN A) L B) T C) S D) T | CE C ENGT YPE: TRAN | HARA H: 3 nuc DEDN: | ID CTER 15 b. leic ESS: unki | ISTIC ase p acic unk nown | CS: pair: | 5 | | | | | | | |
| | | (1 | A) N. B) L | AME/I | | CDS 4 | | SEQ I | ID NO | 0:11 | : | | | | | |
| CAT | ATG Met 1 | | | | | CAA Gln | | | | | | | | | | 48 |
| CAC His | AAA Lys | GGA Gly | ACC Thr | TAC Tyr 20 | TTG Leu | TAC Tyr | AAT Asn | GAC Asp | TGT Cys 25 | CCA Pro | GGC Gly | CCG Pro | GGG Gly | CAG Gln 30 | GAT Asp | 96 |
| | GAC Asp | | | | | | | | | | | | | | | 144 |
| | CTC Leu | | | | | Ser | | | | | | | | | | 192 |
| CAG Gln | GTG Val 65 | GAG Glu | ATC Ile | TCT Ser | TCT Ser | TGC Cys 70 | ACA Thr | GTG Val | GAC Asp | CGG Arg | GAC Asp 75 | ACC Thr | GTG Val | TGT Cys | GGC Gly | 240 |
| TGC Cys 80 | AGG Arg | AAG Lys | AAC Asn | CAG Gln | TAC Tyr 85 | CGG Arg | CAT His | TAT Tyr | TGG Trp | AGT Ser 90 | GAA Glu | AAC Asn | CTT Leu | TTC Phe | CAG Gln 95 | 288 |
| | TTC Phe | | | | | TAA * | AAGC | TT | | | | | | | | 315 |

| (2) | INF | ORMAT | rion | FOR | SEQ | ID 1 | NO:12 | 2: | | | | | | | | |
|-----------|-----------|------------|-------------------------|----------------------|------------------------|-----------------------|----------------------|-------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|----|
| | | (i) S | (A) | | NGTH: | : 102 amino | 2 am: | ino a id | | 5 | | | | | | |
| | (: | ii) N | OLE | CULE | TYPE | E: pi | rote | in | | | | | | | | |
| | (2 | xi) S | SEQUE | ENCE | DESC | CRIP | NOI | : SE | Q ID | NO: | 12: | | | | | |
| Met 1 | Tyr | Ile | His | Pro 5 | Gln | Asn | Asn | Ser | Ile 10 | Cys | Суз | Thr | Lys | Cys 15 | His | |
| Lys | Gly | Thr | Tyr 20 | Leu | Tyr | Asn | Asp | Cys 25 | Pro | Gly | Pro | Gly | Gln 30 | Asp | Thr | |
| Asp | Cys | Arg 35 | Glu | Cys | Glu | Ser | Gly 40 | Ser | Phe | Thr | Ala | Ser 45 | Glu | Asn | His | |
| Leu | Arg 50 | His | Cys | Leu | Ser | Cys 55 | Ser | Lys | Cys | Arg | Lys 60 | Glu | Met | Gly | Gln | |
| Val 65 | Glu | Ile | Ser | Ser | Cys 70 | Thr | Val | Asp | Arg | Asp 75 | Thr | Val | Cys | Gly | Cys 80 | |
| Arg | Lys | Asn | Gln | Tyr 85 | Arg | His | Tyr | Trp | Ser 90 | Glu | Asn | Leu | Phe | Gln 95 | Cys | |
| Phe | Asn | Cys | Ser 100 | Leu | * | | | | | | | | | | | |
| (2) | INF | ORMA' | rion | FOR | SEQ | ID 1 | NO:1 | 3: | | | | | | | | |
| | (i | () | A) L: B) T' C) S' | | H: 2: nuc. DEDNI | 94 ba leic ESS: | ase p acio unk | pair: d | S | | | | | | | |
| | (ii |) MO | LECU: | LE T | YPE: | CDN | A | | | | | | | | | |
| | (ix | • | A) N. | E: AME/I OCAT: | | - | | | | | | | | | | |
| | (xi |) SE | QUEN | CE DI | ESCR: | IPTI | : : NC | SEQ | ID N | 0:13 | : | | | | | |
| CAT | | TCG Ser | | | | | | | | | | | | | | 48 |

AAT GAC TGT CCA GGC CCG GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG
Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu
20 25 30

| - | _ | | | | | | | | CTC Leu | | 144 |
|------|-----|-----|--|------------|--|--|---|--|------------|----------------|-----|
| | | | | | | | | | TCT Ser | | 192 |
| | | Asp | | | | | | | TAC Tyr | | 240 |
| | | | | CTT Leu | | | | | CTG Leu | TAA * 95 | 288 |
| AAGO | CTT | | | | | | , | | | | 294 |

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Ser Ile Ser Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn 1 10 15

Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser 20 25 30

Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys $35 \hspace{1cm} 40 \hspace{1cm} 45$

Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr 50 55 60

Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His 65 70 . 75 80

Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu * 85 90 95

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Asn Ser Ile Cys

- (2) INFORMATION FOR SEQ ID NO:16:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Asn Asn Ser Ile Cys 1 5

- (2) INFORMATION FOR SEQ ID NO:17:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Gln Asn Asn Ser Ile Cys

- (2) INFORMATION FOR SEQ ID NO:18:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Pro Gln Asn Asn Ser Ile Cys 1 5

- (2) INFORMATION FOR SEQ ID NO:19:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

His Pro Gln Asn Asn Ser Ile Cys 1 5

- (2) INFORMATION FOR SEQ ID NO:20:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ile His Pro Gln Asn Asn Ser Ile Cys 1

- (2) INFORMATION FOR SEQ ID NO:21:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Tyr Ile His Pro Gln Asn Asn Ser Ile Cys 1 5 10

- (2) INFORMATION FOR SEQ ID NO:22:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys 1 5 10

- (2) INFORMATION FOR SEQ ID NO:23:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys 1 5 10

- (2) INFORMATION FOR SEQ ID NO:24:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys 1 5 10

- (2) INFORMATION FOR SEQ ID NO:25:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys 1 $$ 5 $$ 10

| (2) | INFOR | MATION FOR SEQ ID NO:26: | | | | | | | |
|-----|----------|---|-----------|-----|-----|-----|-----|-----------|-----|
| | (i) | SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown | | | | | | | |
| | (ii) | MOLECULE TYPE: protein | | | | | | | |
| | (xi) | SEQUENCE DESCRIPTION: SEQ ID NO | :26: | | | | | | |
| | Cys 1 | Pro Gln Gly Lys Tyr Ile His Pro 5 | Gln 10 | Asn | Asn | Ser | Ile | Cys 15 | |
| (2) | INFO | RMATION FOR SEQ ID NO:27: | | | | | | | |
| | (i) | SEQUENCE CHARACTERISTICS: (A) LENGTH: 16 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown | | | | | | | |
| | (ii) | MOLECULE TYPE: protein | | | | | | | |
| | (xi) | SEQUENCE DESCRIPTION: SEQ ID NO | :27: | | | | | | |
| | Val 1 | Cys Pro Gln Gly Lys Tyr Ile His 5 | Pro 10 | Gln | Asn | Asn | Ser | Ile 15 | Cys |
| (2) | INFO | RMATION FOR SEQ ID NO:28: | | | | | | | |
| | (i) | SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown | | | | | | | |
| | (ii) | MOLECULE TYPE: protein | | | | | | | |
| | (xi) | SEQUENCE DESCRIPTION: SEQ ID NO | :28: | | | | | | |
| | Ser 1 | Val Cys Pro Gln Gly Lys Tyr Ile | His 10 | Pro | Gln | Asn | Asn | Ser 15 | Ile |

Cys

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser 1 5 10 15

Ile Cys

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Phe Cys Cys Ser

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Phe Cys Cys Ser Leu 1 5

| (2) | INFOR | OITAM | N FOR | SEQ I | D NO | 0:32 | : | | | | | | | | |
|------------|------------|-------------------|--|-------------------------|----------------------|----------------------|------------------|------------------|------------|------------|------------|------------------|------------------|------------|----|
| | (i) | (A) (B) (C) | ENCE CH. LENGTH TYPE: STRAND TOPOLO | : 6 a amino EDNES | mino ac: SS: v | o ac: id unkno | ids | | | | | | | | |
| | (ii) | MOLEC | CULE TY | PE: p | orote | ein | | | | | | | | | |
| | (xi) | SEQUE | ENCE DE | SCRIE | PTIO | N: S | EQ I | D NO | :32: | | | | | | |
| | Phe 1 | Cys (| Cys Ser | Leu 5 | Cys | | | | | | • | | | | |
| (2) | INFO | RMATIO | ON FOR | SEQ : | ID N | 0:33 | : | | | | | | | | |
| | (i) | (A) (B) (C) | ENCE CH LENGTH TYPE: STRAND TOPOLC | : 7 a amino EDNE: | amin o ac SS: | o ac id unkn | ids | | | | | | | | |
| | (ii) | MOLE | CULE TY | PE:] | prot | ein | | | | | | | | | |
| | (xi) | SEQU | ENCE DE | SCRI | PTIO | N: S | EQ I | D NO | :33: | | | | | | |
| | | Cys | Cys Ser | | Cys | Leu | | | | | | | | | |
| | 1 | | | 5 | | | | | | | | | | | |
| (2) | INFO | RMATI | ON FOR | SEQ | ID N | 0:34 | : | | | | | | | | |
| | (i) | (A) (B) (C) | ENCE CH LENGTH TYPE: STRANI TOPOLO | i: 70 nucl EDNE | 5 ba eic SS: | se p acid unkn | airs l | 3 | | | | | | | |
| | (ii) | MOLE | CULE TY | YPE: | CDNA | | | | | | | | | | |
| | (ix) | | URE: NAME/F LOCATI | | | | | | | | | | | | |
| | (xi) | SEQU | ENCE DE | ESCRI | PTIC | วท: ร | SEQ I | D NO | 34 | : | | | | | |
| TTC Leu | 1 Pro | GCC C Ala G | AG GTG In Val | GCA Ala | TTT Phe | ACA Thr | CCC Pro | TAC Tyr 10 | GCC Ala | CCG Pro | GAG Glu | CCC Pro | GGG Gly 15 | AGC Ser | 48 |
| AC# Thi | TGC Cys | CGG C | TC AGA eu Arg 20 | GAA Glu | TAC Tyr | TAT Tyr | GAC Asp 25 | CAG Gln | ACA Thr | GCT Ala | CAG Gln | ATG Met 30 | TGC Cys | TGC Cys | 96 |

| AGC Ser | AAG Lys | TGC Cys 35 | TCG Ser | CCG Pro | GGC Gly | CAA Gln | CAT His 40 | GCA Ala | AAA Lys | GTC Val | TTC Phe | TGT Cys 45 | ACC Thr | AAG Lys | ACC Thr | 144 |
|--------------------|-------------------|--------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----|
| TCG Ser | GAC Asp 50 | ACC Thr | GTG Val | TGT Cys | GAC Asp | TCC Ser 55 | TGT Cys | GAG Glu | GAC Asp | AGC Ser | ACA Thr 60 | TAC Tyr | ACC Thr | CAG Gln | CTC Leu | 192 |
| TGG Trp 65 | AAC Asn | TGG Trp | GTT Val | CCC Pro | GAG Glu 70 | TGC Cys | TTG Leu | AGC Ser | TGT Cys | GGC Gly 75 | TCC Ser | CGC Arg | TGT Cys | AGC Ser | TCT Ser 80 | 240 |
| GAC Asp | CAG Gln | GTG Val | GAA Glu | ACT Thr 85 | CAA Gln | GCC Ala | TGC Cys | ACT Thr | CGG Arg 90 | GAA Glu | CAG Gln | AAC Asn | CGC Arg | ATC Ile 95 | TGC Cys | 288 |
| ACC Thr | TGC Cys | AGG Arg | CCC Pro 100 | GGC Gly | TGG Trp | TAC Tyr | TGC Cys | GCG Ala 105 | CTG Leu | AGC Ser | AAG Lys | CAG Gln | GAG Glu 110 | GGG Gly | TGC Cys | 336 |
| CGG A rg | CTG Leu | TGC Cys 115 | GCG Ala | CCG Pro | CTG Leu | CGC Arg | AAG Lys 120 | TGC Cys | CGC Arg | CCG Pro | GGC Gly | TTC Phe 125 | GGC Gly | GTG Val | GCC Ala | 384 |
| AGA Arg | CCA Pro 130 | GGA Gly | ACT Thr | GAA Glu | ACA Thr | TCA Ser 135 | GAC Asp | GTG Val | GTG Val | TGC Cys | AAG Lys 140 | CCC Pro | TGT Cys | GCC Ala | CCG Pro | 432 |
| GGG Gly 145 | ACG Thr | TTC Phe | TCC Ser | AAC Asn | ACG Thr 150 | ACT Thr | TCA Ser | TCC Ser | ACG Thr | GAT Asp 155 | ATT Ile | TGC Cys | AGG Arg | CCC Pro | CAC His 160 | 480 |
| CAG Gln | ATC Ile | TGT Cys | AAC Asn | GTG Val 165 | GTG Val | GCC Ala | ATC Ile | CCT Pro | GGG Gly 170 | AAT Asn | GCA Ala | AGC Ser | AGG Arg | GAT Asp 175 | GCA Ala | 528 |
| GTC Val | TGC Cys | A CG Thr | TCC Ser 180 | ACG Thr | TCC Ser | CCC Pro | ACC Thr | CGG Arg 185 | AGT Ser | ATG Met | GCC Ala | CCA Pro | GGG Gly 190 | GCA Ala | GTA Val | 576 |
| CAC His | TTA Leu | CCC Pro 195 | Gln | CCA Pro | GTG Val | TCC Ser | ACA Thr 200 | Arg | TCC Ser | CAA Gln | CAC His | ACG Thr 205 | CAG Gln | CCA Pro | ACT Thr | 624 |
| CCA Pro | GAA Glu 210 | Pro | A GC Ser | ACT Thr | GCT Ala | CCA Pro 215 | AGC Ser | ACC Thr | TCC Ser | TTC Phe | CTG Leu 220 | CTC Leu | CCA Pro | ATG Met | GGC Gly | 672 |
| | Ser | | | | GAA Glu 230 | Gly | | | | | | | | | | 705 |

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 235 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser 1 5 10 15

Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys 20 25 30

Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr 35 40 45

Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu 50 60

Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser 65 70 75 80

Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys 85 90 95

Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys 100 105 110

Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala 115 120 125

Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro 130 135 140

Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His 145 150 155 160

Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Arg Asp Ala 165 170 175

Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val 180 - 185 190

His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr 195 200 205

Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly 210 215 220

Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp 225 230 235

- (2) INFORMATION FOR SEQ ID NO:36:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Ala Gln Met Cys

- (2) INFORMATION FOR SEQ ID NO:37:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Thr Ala Gln Met Cys
1 5

- (2) INFORMATION FOR SEQ ID NO:38:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Gln Thr Ala Gln Met Cys
1 5

- (2) INFORMATION FOR SEQ ID NO:39:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Asp Gln Thr Ala Gln Met Cys
1 5

- (2) INFORMATION FOR SEQ ID NO:40:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Tyr Asp Gln Thr Ala Gln Met Cys 1 $\,$ 5

- (2) INFORMATION FOR SEQ ID NO:41:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Tyr Tyr Asp Gln Thr Ala Gln Met Cys 1

- (2) INFORMATION FOR SEQ ID NO:42:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys 1 $$ 5 $$ 10

- (2) INFORMATION FOR SEQ ID NO:43:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys
1 10

- (2) INFORMATION FOR SEQ ID NO:44:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys 1 5 10

- (2) INFORMATION FOR SEQ ID NO:45:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys 1 $$ 5 $$ 10

- (2) INFORMATION FOR SEQ ID NO:46:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

| | (ii) | MOLECULE TYPE: protein |
|-----|----------|---|
| | (xi) | SEQUENCE DESCRIPTION: SEQ ID NO:46: |
| | Cys 1 | Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys 5 10 |
| (2) | INFO | RMATION FOR SEQ ID NO:47: |
| | (i) | SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown |
| | (ii) | MOLECULE TYPE: protein |
| | (xi) | SEQUENCE DESCRIPTION: SEQ ID NO:47: |
| | Thr 1 | Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys 5 10 15 |
| (2) | INFO | RMATION FOR SEQ ID NO:48: |
| | (i) | SEQUENCE CHARACTERISTICS: (A) LENGTH: 16 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown |
| | (ii) | MOLECULE TYPE: protein |
| | (xi) | SEQUENCE DESCRIPTION: SEQ ID NO:48: |
| | Ser 1 | Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys 5 10 15 |
| (2) | INFO | RMATION FOR SEQ ID NO:49: |
| | (i) | SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown |

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met
1 10 15

Cys

- (2) INFORMATION FOR SEQ ID NO:50:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln 1 $$ 5 $$ 10 $$ 15

Met Cys

- (2) INFORMATION FOR SEQ ID NO:51:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala 1 5 10 15

Gln Met Cys

- (2) INFORMATION FOR SEQ ID NO:52:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr 1 10 15

Ala Gln Met Cys 20

- (2) INFORMATION FOR SEQ ID NO:53:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln 1 5 10 15

Thr Ala Gln Met Cys

- (2) INFORMATION FOR SEQ ID NO:54:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp 1 10 15

Gln Thr Ala Gln Met Cys 20

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr 1 5 10 15

Asp Gln Thr Ala Gln Met Cys 20

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr 1 5 10 15

Tyr Asp Gln Thr Ala Gln Met Cys
20

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu 1 5 10 15

Tyr Tyr Asp Gln Thr Ala Gln Met Cys
20 25

| (2) | INFORMATION | FOR | SEQ | ID | NO:58 |
|-----|-------------|-----|-----|----|-------|
|-----|-------------|-----|-----|----|-------|

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg 1 5 10 15

Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys 20 25

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu 1 5 10 15

Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg
1 10 15

Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys
20 25

| | (2) | INFORMATION | FOR | SEO | ID | NO:61 |
|--|-----|-------------|-----|-----|----|-------|
|--|-----|-------------|-----|-----|----|-------|

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr 1 5 10 15

Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys
20 25 30

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser 1 5 10 15

Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys 20 25 30

- (2) INFORMATION FOR SEQ ID NO:64:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Ala Pro Leu Arg

(i) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:65:

- (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Ala Pro Leu Arg Lys 1 5

- (2) INFORMATION FOR SEQ ID NO:66:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Ala Pro Leu Arg Lys Cys

(2) INFORMATION FOR SEQ ID NO:67:

| | (i) | SEQUENCE CHARACTERISTICS: (A) LENGTH: 7 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown | |
|------|----------|--|----|
| | (ii) | MOLECULE TYPE: protein | |
| | (xi) | SEQUENCE DESCRIPTION: SEQ ID NO:67: | |
| | Ala 1 | Pro Leu Arg Lys Cys Arg 5 | |
| (2) | INFO | RMATION FOR SEQ ID NO:68: | |
| | (i) | SEQUENCE CHARACTERISTICS: (A) LENGTH: 31 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown | |
| | (ii) | MOLECULE TYPE: cDNA | |
| | (xi) | SEQUENCE DESCRIPTION: SEQ ID NO:68: | |
| GGTT | ragcc. | AT ATGGACAGCG TTTGCCCCCA A | 31 |
| (2) | INFO | RMATION FOR SEQ ID NO:69: | |
| | (i) | SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown | |
| | (ii) | MOLECULE TYPE: cDNA | |
| | (xi) | SEQUENCE DESCRIPTION: SEQ ID NO:69: | |
| CCC | AAGCT | TT TACAGAGAGC AATTGAAGCA CTG | 33 |

| (2) | INFO | RMATION FOR SEQ ID NO:/U: | |
|-----|--------|--|----|
| | (i) | SEQUENCE CHARACTERISTICS: (A) LENGTH: 40 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown | |
| | (ii) | MOLECULE TYPE: cDNA | |
| | (xi) | SEQUENCE DESCRIPTION: SEQ ID NO:70: | |
| ACT | CGAGG. | AT CCGCGGATAA ATAAGTAACG ATCCGGTCCA | 40 |
| (2) | INFO | RMATION FOR SEQ ID NO:71: | |
| | (i) | SEQUENCE CHARACTERISTICS: (A) LENGTH: 41 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown | |
| | (ii) | MOLECULE TYPE: cDNA | |
| | (xi) | SEQUENCE DESCRIPTION: SEQ ID NO:71: | |
| CAG | GTCGG | AT CCTATCAGCA GAAGCACTGG AAAAGGTTTT C | 41 |
| (2) | INFO | RMATION FOR SEQ ID NO:72: | |
| | (i) | SEQUENCE CHARACTERISTICS: (A) LENGTH: 31 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown | |
| | (ii) | MOLECULE TYPE: cDNA | |
| | (xi) | SEQUENCE DESCRIPTION: SEQ ID NO:72: | |
| GGT | TAGCC | AT ATGGACAGCG TTTGCGCCCA A | 31 |
| (2) | INFO | RMATION FOR SEQ ID NO:73: | |
| | (i) | SEQUENCE CHARACTERISTICS: (A) LENGTH: 34 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown | |
| | (ii) | MOLECULE TYPE: cDNA | |

| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73: | |
|--|----|
| CGCGGATCCC TATTAATTGA AGCACTGGAA AAGG | 34 |
| (2) INFORMATION FOR SEQ ID NO:74: | |
| (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 30 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: unknown(D) TOPOLOGY: unknown | |
| (ii) MOLECULE TYPE: cDNA | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74: | |
| CCCCATATGT ATATCCACCC TCAAAATAAT | 30 |
| (2) INFORMATION FOR SEQ ID NO:75: | |
| (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 33 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: unknown(D) TOPOLOGY: unknown | |
| (ii) MOLECULE TYPE: cDNA | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75: | |
| CCCAAGCTTT TACAGAGAGC AATTGAAGCA CTG | 33 |
| (2) INFORMATION FOR SEQ ID NO:76: | |
| (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 38 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: unknown(D) TOPOLOGY: unknown | |
| (ii) MOLECULE TYPE: cDNA | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76: | |
| CCCCATATGT CGATTAGCTG TACCAAGTGC CACAAAGG | 38 |

| (2) INFORMATION FOR SEQ ID NO:77: | |
|--|----|
| (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 33 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: unknown(D) TOPOLOGY: unknown | |
| (ii) MOLECULE TYPE: cDNA | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77: | |
| CCCAAGCTTT TACAGAGAGC AATTGAAGCA CTG | 33 |
| (2) INFORMATION FOR SEQ ID NO:78: | |
| (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 30 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: unknown(D) TOPOLOGY: unknown | |
| (ii) MOLECULE TYPE: cDNA | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78: | |
| CCCCATATGT GTACCAAGTG CCACAAAGGA | 30 |
| (2) INFORMATION FOR SEQ ID NO:79: | |
| (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 33 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: unknown(D) TOPOLOGY: unknown | |
| (ii) MOLECULE TYPE: cDNA | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79: | |
| | |
| CCCAAGCTTT TACAGAGAGC AATTGAAGCA CTG | 33 |
| | 33 |
| CCCAAGCTTT TACAGAGAGC AATTGAAGCA CTG | 33 |

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| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80: | |
|--|----|
| GGTTAGCCAT ATGGACAGCG TTTGCCCCCA A | 31 |
| (2) INFORMATION FOR SEQ ID NO:81: | |
| (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 33 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: unknown(D) TOPOLOGY: unknown | |
| (ii) MOLECULE TYPE: cDNA | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81: | |
| CCCAAGCTTT TAGGTGCACA CGGTGTTCTG TTT | 33 |